REMARKS

Reconsideration of the application in view of the above amendments and following remarks is requested. Claims 1-8, 10, and 25-35 are now in the case. Claims 1 and 25 - 29 have been amended using language suggested by the Examiner. Support for this language is in the claims as filed. Accordingly, Applicant asserts that the present amendment adds no new matter. Applicant reserves the right to prosecute claims to cancelled subject matter in one or more continuing applications.

THE §112, SECOND PARAGRAPH REJECTION

The Examiner has rejected claims 1-8, 10 and 25-29 under 35 U.S.C. §112, second paragraph as being indefinite because the recitation of "at an epitope within a polypeptide consisting of at least one of amino acids ....". Claim 1 has been amended to more clearly define the epitopes that the antibody bind to as suggested by the Examiner.

Claims 28 and 29 have also been amended to be independent claims. It is believed that these amendments overcome the objection to the claims as indefinite and withdrawal of the rejection on this grounds is respectfully requested.

THE §112, FIRST PARAGRAPH REJECTIONS

The Examiner has rejected claims 1-8, 10 and 25-29 under 35 U.S.C. §112, first paragraph, stating that the claims contain subject matter which was not described in a way as to reasonably convey to one skilled in the art that the inventors, at the time of filing, possessed the claimed invention. The claims have been amended as suggested by the Examiner with one difference – the sequence used for the binding of BCMA is the amino acid 1 to 54 fragment, with amino acid 13 to 27 fragment as a dependent claim. The disclosure of the 1 to 54 fragment and its subfragment occurs in several places throughout the specification, for example, page 16, lines 25-27.

It is alleged that the amendments to the claims, filed February 26, 2006, have introduced new matter. Although Applicants do not agree with this conclusion, the claims have been amended as suggested in the action to speed prosecution. A further objection, the amendment to claims 28 and 29 for insufficient written support is now moot given the language suggested by the Examiner and the support at page 4, lines 22-26.

The 35 U.S.C. §103(a) Rejection

The Examiner has rejected claims 1-8 and 26-29 under 35 U.S.C. §103(a) as unpatentable over Theill et al. (U.S. Patent No. 6,774,106) in view of Gross et al. (WO 00/40716). More specifically, it is alleged that it would have been obvious to one skilled in the art to have produced a method of inhibiting tumor cell proliferation comprising administering a composition or pharmaceutical composition comprising an antibody that binds BCMA and TACI, wherein binding to TACI is within the cysteine rich domains and the BCMA-TACI antibody is conjugated to a therapeutic or diagnostic agent for therapeutic benefit in lymphoma patients. This rejection is respectfully traversed.

It is respectfully submitted that Gross et al. does not teach the specific fragment (amino acids 1 to 54) nor subfragment (amino acids 13 to 27) of BCMA claimed in this patent and it would not be obvious to one of ordinary skill that using a larger or smaller subfragment of this molecule as an epitope would result in an antibody that would bind both TACI and BCMA. Because of the lack of this teaching, the present rejection does not render the present claims obvious, and is rightfully withdrawn.

Furthermore, the presently claimed antibodies are an unexpected result of screening antibodies that bound well to the TACI molecule for ability to bind BCMA. This is an unexpected because the homology between the TACI cysteine repeat and the BCMA cysteine repeat is not great – only on the order of 32.3% identity (see attached FASTA printout). This lack of homology would teach one of ordinary skill away, rather than toward, the claimed method and would lead one of ordinary skill to believe that this antibody would be a difficult thing to obtain. However, given the extra guidance of the present specification, this antibody is something that can be produced. Because of the unexpected nature of this result and the relative difficulty of getting such a result without the specific teachings of the present specification, the present method cannot be considered obvious, and this rejection is properly overcome.

On the basis of the above amendments and remarks, Applicant believes that each rejection has been addressed and overcome. Reconsideration of the application and its allowance are requested. If for any reason the Examiner feels that a telephone conference would expedite prosecution of the application, the Examiner is invited to telephone the undersigned at (206) 442-6752.

Please charge any additional fee required or credit any overpayment to Deposit Account No. 26-0290.

Respectfully Submitted,

Michelle L Lewis

Michelle L. Lewis
Registration No. 36,352

Enclosures:
Petition and Fee for Extension of Time
FASTA printout
Customer No. 10117
ZymoGenetics, Inc.

```
warning ktup = 6 out of range [1..2], reset to 2
# /usr/local/bin/fasta3 -
w 100 /tmp/fseq_file1169253370 /tmp/fseq_file1169253367 6
FASTA searches a protein or DNA sequence data bank
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

Query library /tmp/fseq_file1169253370 vs /tmp/fseq_file1169253367 libra
ry
searching /tmp/fseq_file1169253367 library

  1>>>TACI Cysteine Rich repeat - 33 aa

     34 residues in     1 sequences
 Altschul/Gish params: n0: 33 Lambda: 0.158 K: 0.019 H: 0.100

FASTA (3.47 Mar 2004) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 36, opt: 24, open/ext: -10/-2, width:  16
 Scan time:  0.001
The best scores are:
                           opt bits E(1)
BCMA Cysteine Rich repeat
                    (  34)   95  34.5 4.7e-08

>>BCMA Cysteine Rich repeat
                           (34 aa)
 initn:  37 init1:  37 opt:  95  Z-score: 177.0  bits: 34.5 E(): 4.7e-08
Smith-
Waterman score: 95;  32.353% identity (64.706% similar) in 34 aa overlap
 (1-33:1-34)

               10        20         30
TACI    CPEEQYWDPLLGTCMSCKTICNHQSQR-TCAAFC
        : ...:.: :: .:. :.  :. ..   ::  .:
BCMA    CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
               10        20        30



33 residues in 1 query   sequences
34 residues in 1 library sequences
 Scomplib [34t25]
 start: Fri Jan 19 16:36:10 2007 done: Fri Jan 19 16:36:10 2007
 Total Scan time:  0.001 Total Display time:  0.000

Function used was FASTA [version 3.4t25 Nov 12, 2004]
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